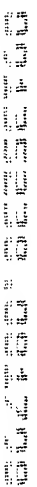
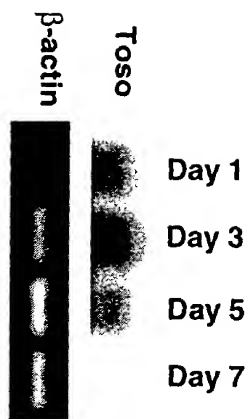


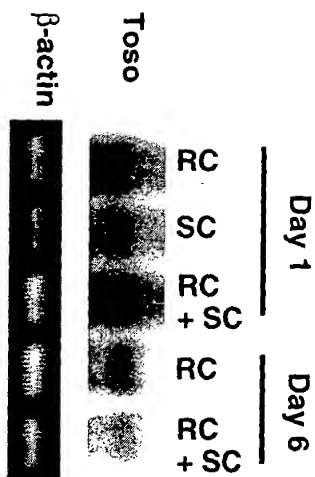
Figure 7

[illegible]

a)



b)



Figur 9

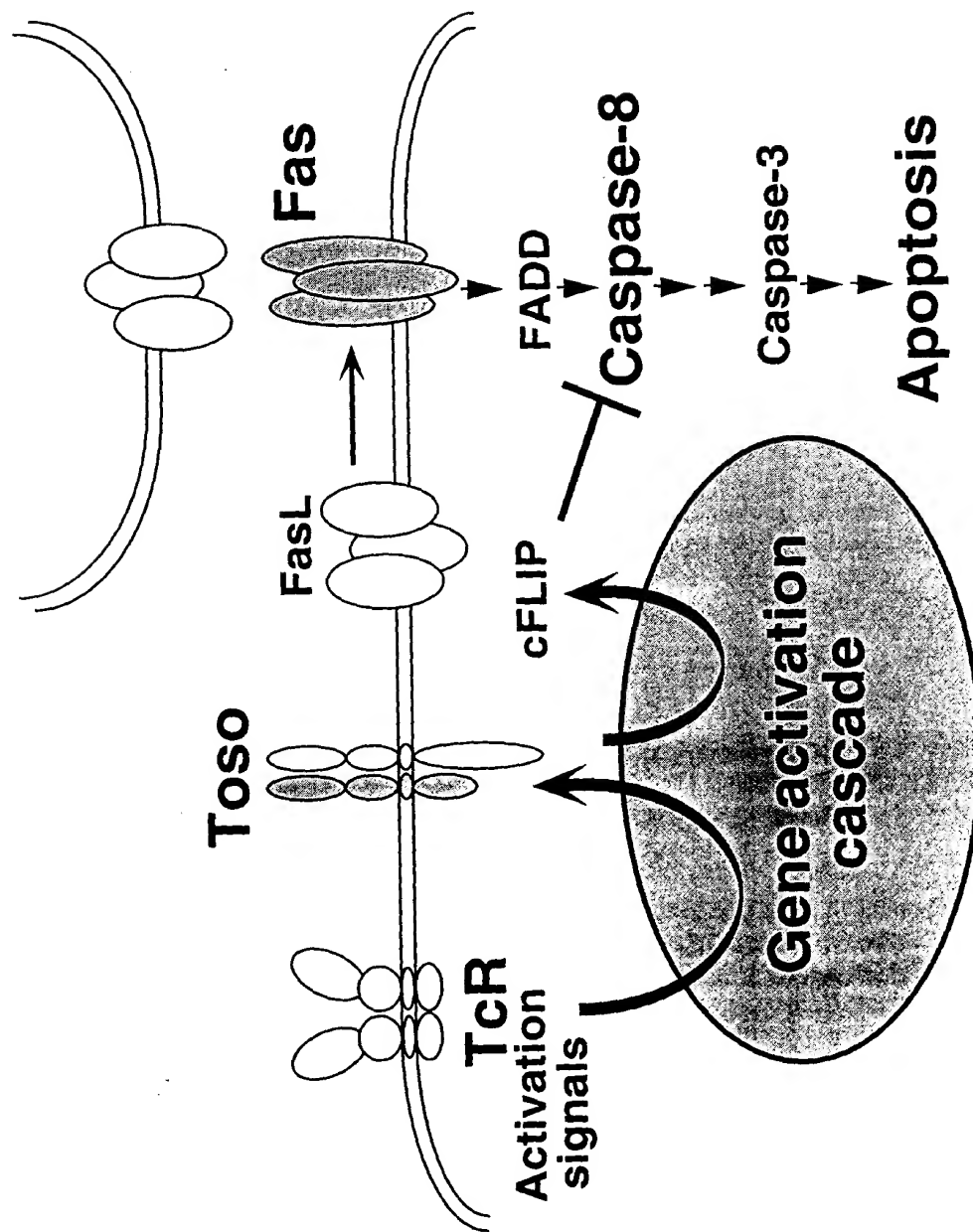
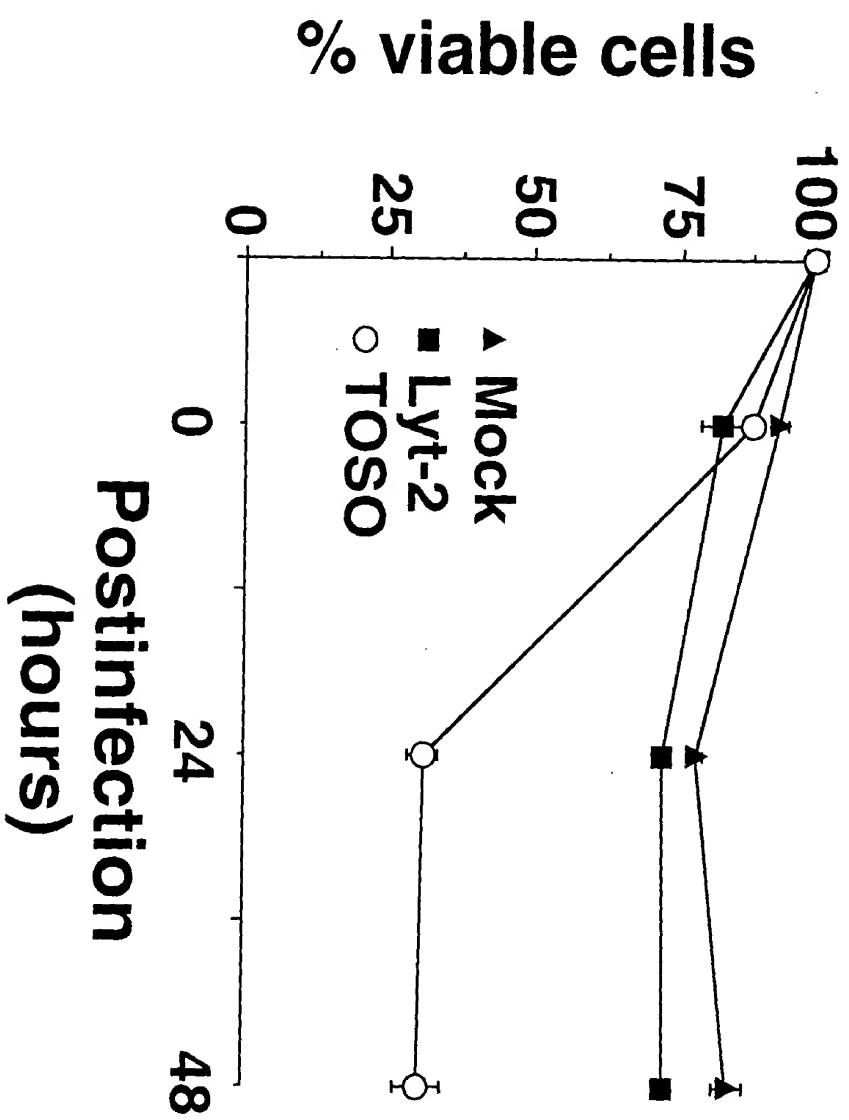


Figure 10

Downloaded from www.sciencedirect.com



100% 4 20 22 24 26 28 30 32 34 36 38 40 42 44 46 48 50 52 54 56 58 60 62 64 66 68 70 72 74 76 78 80 82 84 86 88 90 92 94 96 98 100

Figure 11

aaaggagtaagcagcgtgtctccatccccctctctaggggctcttgg ATGGACCTTGCACTCTAGAAGGGACAATGGACT
TCTGGCTTTGGCCACTTTACTTTCCTGCCAGTATCAGGGGCCCTG AGGATCCTCCCAGAAGTAAAGGTAGAGGGGGAGCTG
 GGCGGATCAGTTACCATCAAATGCCCACTTCCTGAAATGCATGTGAGGATATATCTGTGCCGGGAGATGGCTGGATCTGG
 AACATGTGGTACCGTGGTATCCACCACCAACTTCATCAAGGCAGAATACAAGGGCCGAGTTACTCTGAAGCAATACCCAC
 GCAAGAATCTGTTCTTAGTGGAGGTAACACAGCTGACAGAAAGTGACAGCGGAGTCTATGCCTGCCGAGCGGGCATGAAC
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 tgataaaccaaacttattagcaagatatgcatatatatccataaattctctttactctgtctccatcctt

Coding region: Capitalized

Leader sequence: Underlined

Transmembrane region: Double underlined

Figure 1

1 MDFWLNLXYF LPVSGAL RIL PEVKVEGELG GSATIKCPBP EMHVRITYLCK
51 EMAGSGTCGT VVSTTNFIKA EYGRVTLKQ YPRKNLFLVE VTQLTESDSG
101 VYACGAGMNT DRGKTQKVTL NVHSEHPSW EEQPMPEPK WFHLPLYLQM
151 PAYASSSTKV TRVTPAQRG KVPVHHSSP TTQITHRPV SRASSVAGDK
201 PRFLPSTTA SKISALEGL KPQTPYRNH TRLHRRLALD YGSGVREGQ
251 GPHLLPITLL GLEFLALIGL VVKRAVERKK ALSRRARLA VSRALSSQS
301 RPRGSPRPRS QNNIYSACPR RARGDAAGT GEAPVPGPGA PLPPAPLQVS
351 ESPWLHAPSL KTSCEYVSLY HQPAMMEDS DSDDYINVPA

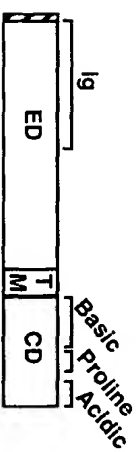


Figure 2

[illegible]

[illegible]

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MEPRYASLRQSCPSQSEQGDDEACALGLIMMGV

351	ESWLEABSLNKBZCIVS	372	QZANMDSDDYINVA
162	DAWMOCHARWYDRCEVLA	192	TEACVVRDANPHERBA
881	QOPLAPPEPSCPEIVNI	928	QZANREBGTGTEETMRODL
349	WEMWDBEALRNLRIGFY		

[illegible]

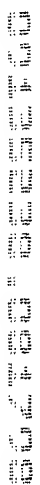


Figure 4

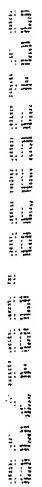
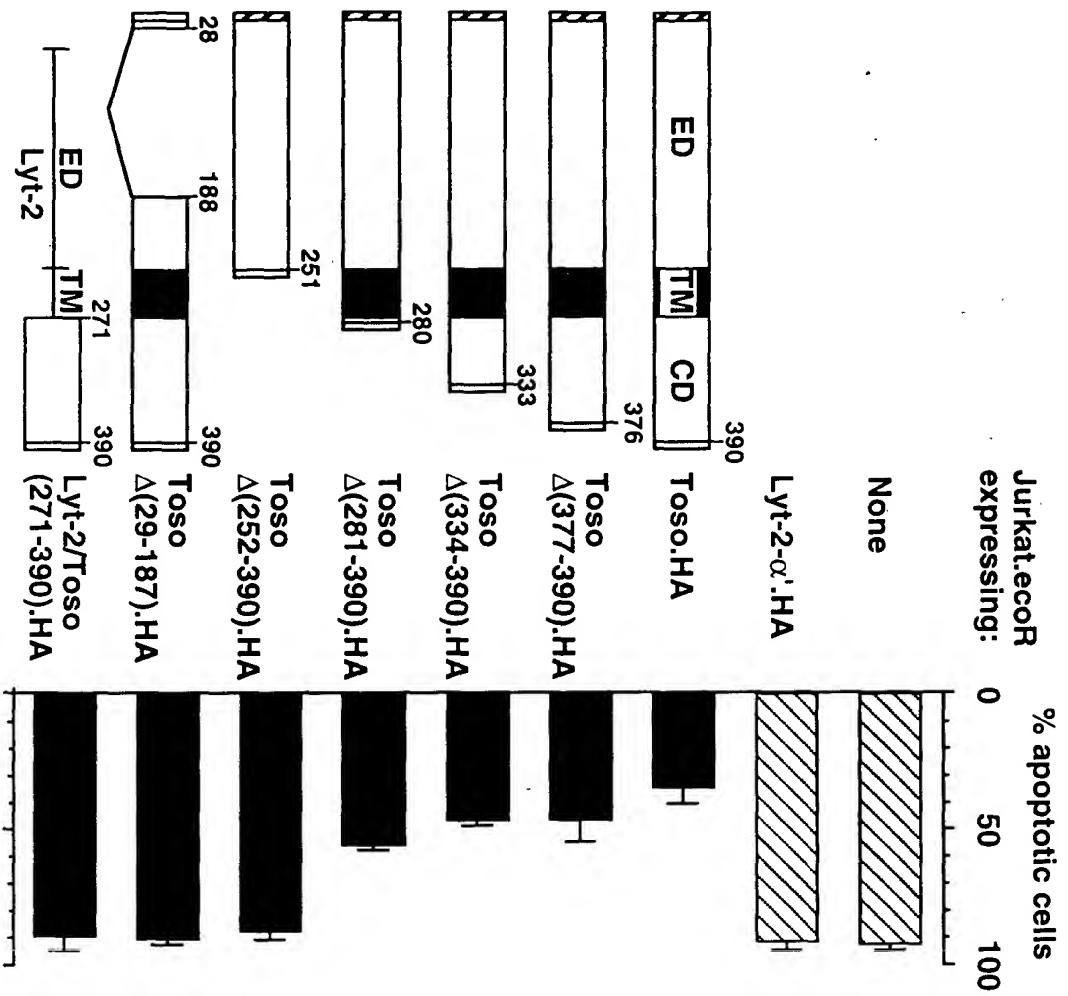


Figure 5

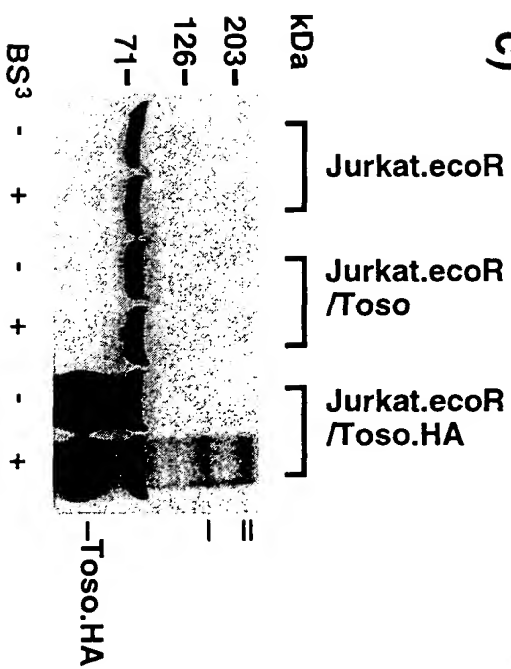
a)



b)



c)



Figur 6